

AMENDMENT TO THE SPECIFICATION

Please amend the paragraph starting on page 3, line 9 according to the following marked-up
5 version. The Applicant hereby requests to replace the original paragraph with this amended
paragraph.

One approach is an iterative dynamical programming method (e.g. *Laurants D.V. et al.*
10 *(1993) Structural similarity of DNA-binding domains of bacteriophage repressors and the globin core. J. Mol. Biol. 3:141-148; and Gerstein M. & Levitt M. (1996) Using iterative dynamic programming to obtain accurate pairwise and multiple alignments of protein structures. In: Proceedings of the 4th International Conference on Intelligent Systems in Molecular Biology, Menlo Park, CA: AAAI Press*). In this approach one first computes a distance matrix between all pairs of atoms (e.g. C_α) forming a similarity matrix, which by
15 dynamical programming methods gives rise to an assignment matrix mimicking the sequence alignment procedure. One of the chains is then moved towards the other by minimizing the distance between assigned pairs. This method does not allow for permutations, since the internal ordering is fixed by construction. In another inter-atomic approach the area rather than the distances between two structures is minimized (e.g. Patent No. 5,878,373). In yet
20 another approach, one compares ~~distances~~ distance matrices within each other of the two structures to be aligned, which provide information about similar structures (e.g. *Holm L. & Sander C. (1993) Protein structure comparison by alignment of distance matrices. J. Mol. Biol. 233:123-138; and Lu G. (2000) A new method for protein structure and similarity*

searches. *J. Appl. Cryst.* *33*:176-183). The similar structures are subsequently matched. In these methods, for instance by Holm & Sander as well as by Lu, permutations can in principle be dealt with.

Please amend the paragraph starting on page 25, line 8 according to the following marked-up version. The Applicant hereby requests to replace the original paragraph with this amended paragraph.

5 It is important to note that while the present invention has been described in the context of a fully functional data processing system and method, those skilled in the art will appreciate that the mechanism of the present invention is capable of being distributed in the form of a computer readable medium of instructions in a variety of forms, and that the present invention applies equally regardless of the particular type of signal bearing medium used to
10 actually carry out the distribution. In other words, the present invention is also a program storage device accessible by a computer, tangible embodying a program of instructions or means executable by the computer to perform method steps for protein structure alignments.
Examples of computer readable medium include: recordable type media such as floppy disks and CD-ROMS and transmission type media such as digital and analog communication
15 links. In addition, the present invention could be implemented and coded in different programming languages such as, but not limited to, for example C and C⁺⁺ programming languages, JAVA or Java script, or DHTML